THE CHROMOSOMES AND RELATIONSHIPS OF METASEQUOIA AND SEQUOIA (TAXODIACEAE): AN UPDATE[1]

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In 1948 Stebbins reported on the chromosome number and relationships of the newly discovered *Metasequoia glyptostroboides* Hu & Cheng ($2n = 2x = 22$) and *Sequoia sempervirens* (D. Don) Endl. ($2n = 6x = 66$). Further research on the karyological relationships between these two taxodiaceous species has not been reported in the following years. The observation of marker chromosomes with unusual structures in various species of Taxodiaceae (Schlarbaum & Tsuchiya, 1975, 1976, 1981) stimulated the authors to investigate the chromosome morphology of *Metasequoia* and *Sequoia* for possible indications of cytotaxonomic and evolutionary relationships. This paper is a brief report addressing only the marker chromosome differences between *Metasequoia* and *Sequoia*. Expanded accounts of the overall karyotypic features of these species will be published elsewhere (Schlarbaum & Tsuchiya, 1984; Schlarbaum *et al.*, 1983).

Interest in the chromosome complement of *Sequoia* developed after Lawson (1904) suspected that the species was polyploid. The chromosome number of *Sequoia* was determined with certainty by the independent meiotic studies of Hirayoshi and Nakamura (1943) and Stebbins (1948). Figure 1 is the previously unpublished photo by Hirayoshi and Nakamura (both now deceased) showing the chromosome configurations from which the hexaploid count was determined. As shown by this photograph and the drawings of microsporocytes by Stebbins (1948) and Hirayoshi and Nakamura (1943), multivalents are present, suggesting that *Sequoia* is at least partially autopolyploid.

Before the discovery of *Metasequoia* was published, some scientists (Jensen & Levan, 1941; Hirayoshi & Nakamura, 1943) speculated whether *Sequoiadendron giganteum* (Lindley) Buchholz, previously classified as *Sequoia gigantea* (Lindley) Decne., may have contributed one or more genomes to *Sequoia*. The discovery of living *Metasequoia* trees naturally stimulated hypotheses involving ancestral relationships between *Metasequoia* and *Sequoia*. These inferences were based upon the morphological similarities between the two species, and probably in part on the previous confusion of fossil remains of *Sequoia* and *Metasequoia* (Miki, 1941; Chaney, 1951). After determining the diploid nature of *Metasequoia*, Stebbins (1948) considered the plausibility

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FIGURE 1. Microsporocyte of *Sequoia sempervirens* showing complete chromosome complement ($2n = 2x = 66$) and various multivalents, × ca. 2200 (Hirayoshi & Nakamura, unpubl.).

of a *Metasequoia* species being a Mesozoic or early Tertiary ancestor of *Sequoia*. More recently, Saylor and Simons (1970) speculated on the possibility of chromosomal relationships between *Metasequoia* and *Sequoia*.

In the present study, observations for marker chromosomes were made on the root-tip mitosis of *Sequoia* and *Metasequoia*. *Sequoia* seeds from an unknown locality were obtained from a commercial company and germinated. *Metasequoia* cuttings were taken from trees originating from the only extant population in western Hubei Province, China, and rooted. Cytological methodology followed Schlarbaum and Tsuchiya (1976). Vouchers are deposited at CS.

Our karyological observations show the presence of marker chromosomes with unusual structures in *Metasequoia* and *Sequoia* (FIGURE 2, a, b). *Metasequoia* has three pairs of chromosomes with long kinetochore regions (FIGURE 2, a). *Sequoia* has two pairs of SAT-chromosomes with long secondary constrictions in which chromomeres are visible, and another chromosome pair that probably has microsatellites attached to the short arm (Schlarbaum, 1980; Schlarbaum & Tsuchiya, 1984) (FIGURE 2, b; microsatellites not visible).

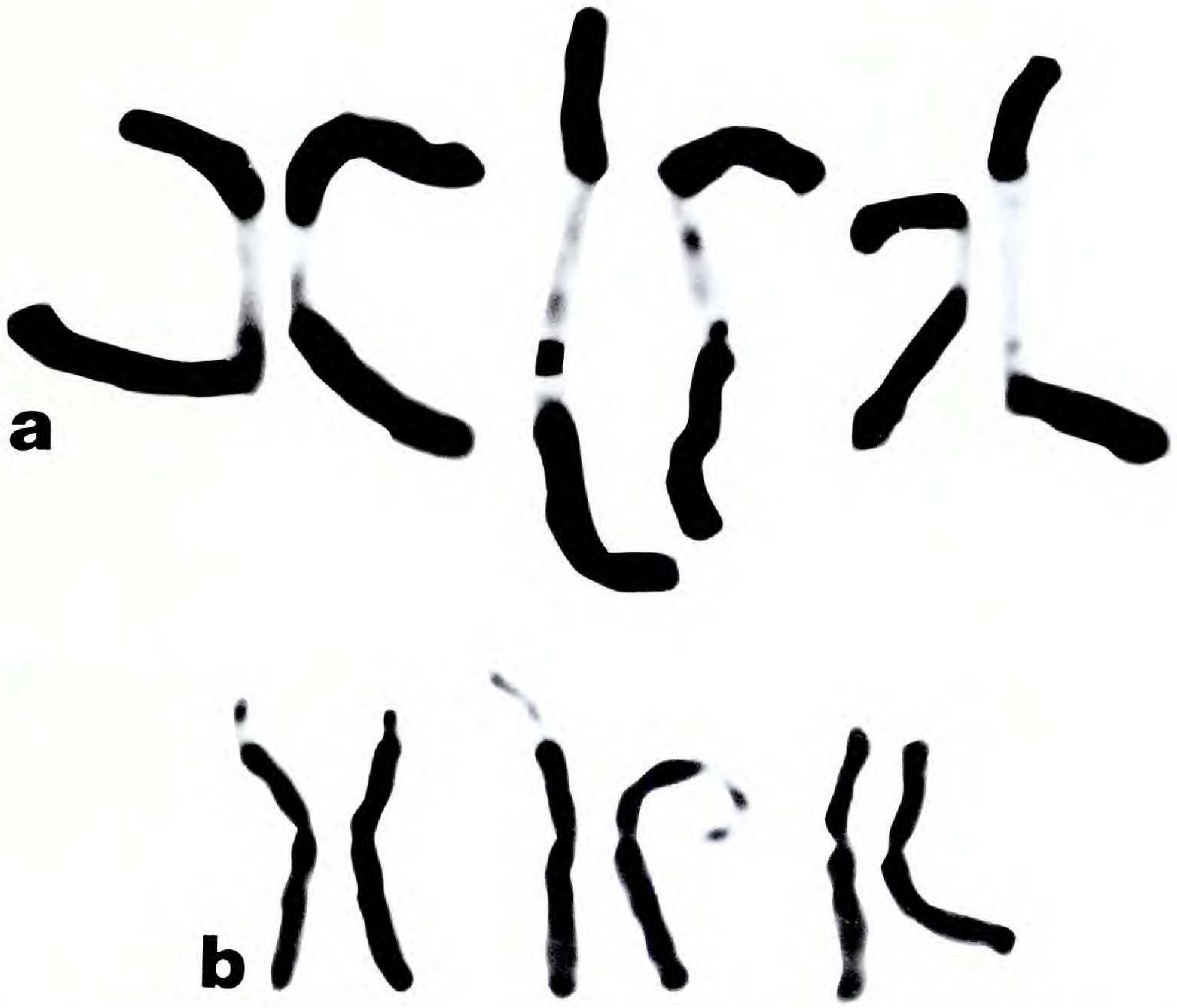

FIGURE 2. Marker chromosome pairs, × 3000: a, *Metasequoia glyptostroboides*, $2n = 2x = 22$, showing long kinetochore regions; b, *Sequoia sempervirens*, $2n = 6x = 66$ (left and center pairs show long secondary constrictions and corresponding satellite bodies).

CONCLUSIONS

The marker chromosome type found in *Metasequoia* was not observed in *Sequoia*, indicating the lack of a direct cytotaxonomic relationship between the two species, although the effects of amphiplasty (Navashin, 1928) cannot be entirely discounted. Based on the cytological evidence presented, genomic contribution of the extant *Metasequoia* species to the polyploidy of *Sequoia* is considered unlikely. It must be recognized that the chromosome studies were conducted on monotypic, relictual genera that undoubtedly contained more species in past geologic epochs. However, the fossil record supports the cytological conclusion that *Sequoia* was differentiated independently from *Metasequoia* but probably came from the same general ancestral stock (Arnold & Lowther, 1955).

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